

FIGURE 1**RTVP and RGL1 α , RGL1 β DNA compare**

RTVP-1	1	CTCTGTTTTCTCAAAGCTGAAGTCGGCTAGGTTTGCAAAGCTGTGGGCTG
RGL α	1	-----
RGL β	1	-----
consensus	1	
RTVP-1	51	AGCACTCAGGCAATCACACTCTCAGAAACTGCGGCGGCTCTGGACTGCAG
RGL α	1	-----CATCCTCCGCATC-CTCCAC---AT
RGL β	1	-----CATCCTCCGCATC-CTCCAC---AT
consensus	51	cAtCctCcGCatC CTccAC At
RTVP-1	101	CCTCCCAAGGCTCCATGCCAGACAAAGCATGCGTGTACACTTGCTACAA
RGL α	22	CCTTCCATGGCTC--TG-----AAGAATAAATT---CAGTTGTTTATG
RGL β	22	CCTTCCATGGCTC--TG-----AAGAATAAATT---CAGTTGTTTATG
consensus	101	CCTtCCAtGGCTC TG AAGaTaaaTt CAgTTGtTtatg
RTVP-1	151	TAGCCTGGATGGTTTCTTTTGTCTCCAATTATTACACACAGCAAATATT
RGL α	60	GATCTTGGGTC-TGTGTTTGGTAGCCACTACATCTTCCA----AAATC--
RGL β	60	GATCTTGGGTC-TGTGTTTGGTAGCCACTACATCTTCCA----AAATC--
consensus	151	gAtCtTGGgTc TgTgTTTgGTagCCAcTacaTcttccAAATc
RTVP-1	201	TTGCCAGATATCGAAAATGAAGATTTTCATCAAAGACTGCGTTTGAATCCA
RGL α	103	---CCATCCATCACTGACCCACACTTTATAGACAACCTGCATAGAAGCCCA
RGL β	103	---CCATCCATCACTGACCCACACTTTATAGACAACCTGCATAGAAGCCCA
consensus	201	CCAtccATCactgAcccAcAcTtTtATagAcaACTGCaTagaAgcCCA
RTVP-1	251	TAACAAGTTCCGATCAGAGGTGAAACCAACAGCCAGTGATATGCTATACA
RGL α	150	CAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACA
RGL β	150	CAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACA
consensus	251	cAACGAAtgGCGtggaAaGTcAAcCctcCcGCggccGAcATGaaATACA
RTVP-1	301	TGACTTGGGACCCAGCACTAGCCCAAATTGCAAAGCATGGGCCAGCAAT
RGL α	200	TGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAG
RGL β	200	TGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAG
consensus	301	TGAtTTGGGAtaaAGgttTAGCaaAgATgGctAAAGCATGGGCAaAcCag
RTVP-1	351	TGCCAGTTTTTCACATAATACACGGCTGAAGCCACCCCAAGCTGC-ACC
RGL α	250	TGCAAATTTGAACATAATGACTGTTTGGATAAATCATATAAA-TGCTATG
RGL β	250	TGCAAATTTGAACATAATGACTGTTTGGATAAATCATATAAA-TGCTATG
consensus	351	TGCaAaTTTgaACATAATgactGttTGgAtaaAtCatAtAaa TGctAtg
RTVP-1	400	CAAACCTTCACTTCACTGGGAGAGAACATCTGGACTGG--GTCTGTGCCCA
RGL α	299	CAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGTGGAATAAAGTCA
RGL β	299	CAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGTGGAATAAAGTCA

consensus 401 CAgctTTtgaaTatgTtGGAGAAAtATCTGGttaGGtgGaaTaaagtCA

RTVP-1 448 TTTTTTCTGTGTCTTCCGCCATCACAACTGGTATGACGAAATCCAGGAC
 RGL α 349 TTCACACCAAGACAT--GCCATTACGGCTTGGTATAATGAAACCCAATTT
 RGL β 349 TTCACACCAAGACAT--GCCATTACGGCTTGGTATAATGAAACCCAATTT
 consensus 451 TTcacaCcaaGaCaT GCCATtACggctTGGTATaAtGAAAcCCAattt

RTVP-1 498 TATGACTTCAAGACTCGGATATGCAAAAAAGTCTGTGGCCACTTACACTCA
 RGL α 397 TATGATTTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACA
 RGL β 397 TATGATTTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACA
 consensus 501 TATGAtTTtgAtAgTCTatcATGctccAgAGTCTGTGGCCatTAtACaCA

RTVP-1 548 GGTGTTTGGGCAGATAGTTACAAAGTTGGCTGCGCAGTTCAATTTTGCC
 RGL α 447 GTTAGTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTC
 RGL β 447 GTTAGTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTC
 consensus 551 GtTaGTTTGGGCcaAttcaTtttAtGTcGGtTgTGCAGTTgcAaTgTgTcC

RTVP-1 598 CTAAAGTTTCTGGCTTTGACGCTCTTTCCAATGGAGCACATTTTATATGC
 RGL α 497 CTAA-----CCTTGGGGGAGCTTCAACTGCAATA---TTTGTATGC
 RGL β 497 CTAA-----CCTTGGGGGAGCTTCAACTGCAATA---TTTGTATGC
 consensus 601 CTAA CcTTGggGgagcTTCaAcTGcAata TTTgTATGC

RTVP-1 648 AACTACGGACCAGGAGGGAATTACCCAAGTTGGCCATATAA---GAGAGG
 RGL α 535 AACTACGGACCTGCAGGAAATTTTGCAAATATGCCTCCTTACGTAAGAGG
 RGL β 535 AACTACGGACCTGCAGGAAATTTTGCAAATATGCCTCCTTACGTAAGAGG
 consensus 651 AACTACGGACcTgcAGGaAATTTtgCAAaTatGCctccTtAcgtaAGAGG

RTVP-1 695 AGCCACCTGCAGTGCCTGCCCCAATAATGACAAGTGTtTGGACAATCTCT
 RGL α 585 AGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTAAAGAACCTCT
 RGL β 585 AGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTAAAGAACCTCT
 consensus 701 AGaatCtTGctcTctCTGctCaAAagAaGAgAAaTGTgTaaAgAAcCTCT

RTVP-1 745 GTGTTAACCGACAGCGAGACCAAGTGAAACGTTACTACTCTGTTGTATAT
 RGL α 635 GCA-----AAAATCCATTTCTGAAG
 RGL β 635 GCAGGACTCCACAAGTTATTATACCTAACC---AAAATCCATTTCTGAAG
 consensus 751 Gca a c acagc g a aa c AaaAtcCatTTcTgaAg

RTVP-1 795 CCAGGCTGGCCCATATATCCACGTAACAGATACACTTCTCTCTTTCTCAT
 RGL α 655 CCAACGGGG-----AGAGCACCTCAGCAGACAGCCTTTAATCCAT-TCAG
 RGL β 682 CCAACGGGG-----AGAGCACCTCAGCAGACAGCCTTTAATCCAT-TCAG
 consensus 801 CCAacggGG AgAgCacCtcAgCAGAcAgcCTTtaaTCcaT TCAG

RTVP-1 845 TGTTAATTCAGTAATTCTAATACTGTCTGTTATAATTACCATTTTGGTAC
 RGL α 699 CTTAGGTTTTCTTCTTCTGAGAAT--CTTTTAATGT---CATTTATATAC
 RGL β 726 CTTAGGTTTTCTTCTTCTGAGAAT--CTTTTAATGT---CATTTATATAC
 consensus 851 ctTaggTtttcTtctTCTgAgAaT CTtTTAatgT CATTTataTAC

RTVP-1 895 AGCTCAAGTACCCTAATTTAGTTCTTTTGGACTAATACAATTCAGGAA-A
 RGL α 744 AAAAGAAATTCTCAAATGT-----TAAAATAAAGGAATA

RGL β 771 AAAAGAAATTCTCAAATGT-----TAAAATAAAGGAATA
 consensus 901 AaaagAAaTtCtCaAATgT TAAaATaaAGGAAtA

RTVP-1 944 GAAAAAACCCAAAAACCAACCTCATTCACATATGGCTTTTTT--TTAACC
 RGL α 778 GTTTATTGCTTAATATAA--CTTATCATCACTTTGCTTCTTTACTGAATC
 RGL β 805 GTTTATTGCTTAATATAA--CTTATCATCACTTTGCTTCTTTACTGAATC
 consensus 951 GtttAttgCttAAtAtaA CTtATcatCActTtGCTTcTTTactGAAAtC

RTVP-1 992 AATAACAATTAGGTGTACTTCTATTTTAAACATTTTCAGAAAAAAATA

RGL α 826 TTCTACACTCTTGC---CTGATACCTAAA----- (SEQ ID NO: 1)

RGL β 853 TTCTACACTCTTGC---CTGATACCTAA----- (SEQ ID NO: 3)

consensus1001 ttctACAcTcttGc CTgaTAccTaAA

FIGURE 2

RTVP-1 and RGL1 α , RGL1 β protein compare

[illegible]

signal peptide	MQVILAVIVWM
SCP-domain(sig1,sig2)	VCGRYTQVVWAD
Caveolin biding site	YNETQFYDF
TM-domain	YTSFLIVNSVILILSVIITILV

FIGURE 3**RGL1 p53 binding sites****(Promoter 4kb--intron 4)**

Intron 1

- 581 AAATAAGTTC AAAACT GTACTAGTCT 90% (A)
- Intron 2
- 1559 AGACTAGTTT CTTAC ATACATGTTT 95% (B)
- 1559 AAGCCTGTTT AAGCAATATAAA GAGCTAACCT
TCTTCTCT AGACTTACCC 90% (C, C2)
- 16403 GAGCTTACTC TTTAT TGGCTAGTTT 90% (D)
- Intron 3
- 3116 AGATAAGTCT GA GGTCTTGTCT 90% (E)
- 32226 AGACAAGCCA CCTGG AAGAAAGTCT 90% (F)
- Intron 4
- 35786 AAACAAACTT T AGACAAGTTT 95% (G)
- 36649 TAACTAGTTT GGGTACTAGTAAACC
TGGCATGCCC TC AAACTTTTTT 90% (H, H2)
- 38942 AGACATTCTC TATA AAGCTATTTT 90% (I)

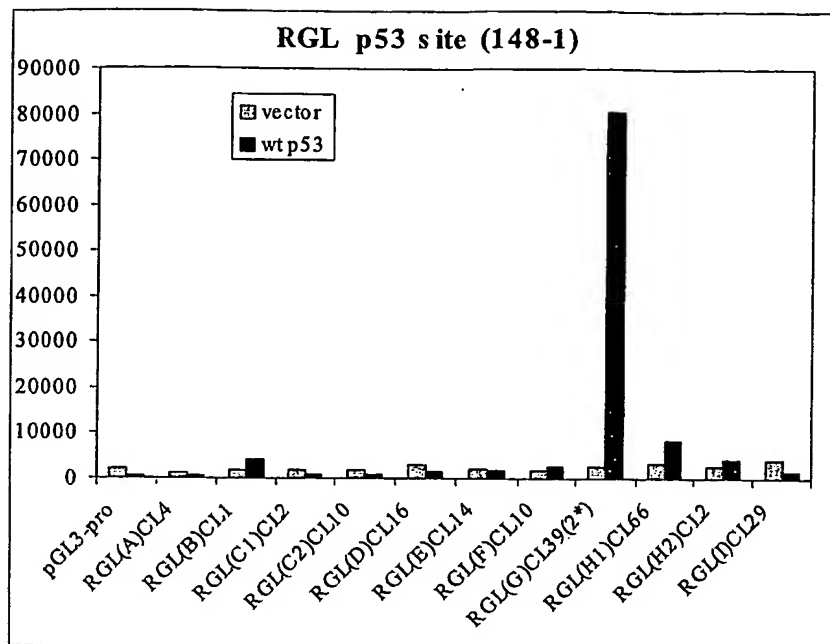
FIGURE 4

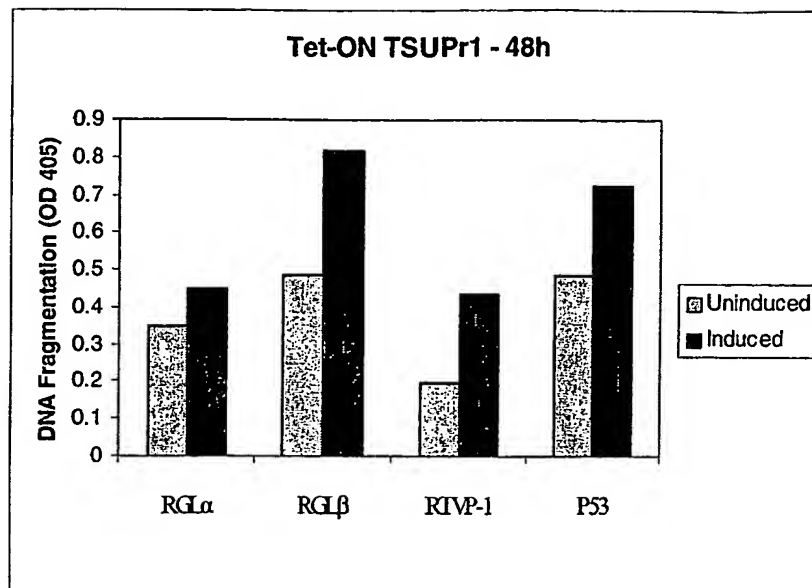
FIGURE 5

FIGURE 6